; Sequence 12, Application US/10030203
; GENERAL INFORMATION:
;   APPLICANT:
;   APPLICANT: Alan Garen
;   APPLICANT: Zhiwei Hu
;   TITLE OF INVENTION: Neovascular-Targeted Immunoconjugates
;   FILE REFERENCE: OCR-679B.US
;   CURRENT APPLICATION NUMBER: US/10/030,203
;   CURRENT FILING DATE: 2001-12-31
;   PRIOR APPLICATION NUMBER: PCT/US00/16481
;   PRIOR FILING DATE: 2000-06-14
;   NUMBER OF SEQ ID NOS: 12
;   SOFTWARE: MS DOS
;
;   SEQ ID NO 12
;   LENGTH: 2138
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: CDS
;   OTHER INFORMATION: hfvIIasm immunoconjugate
;   OTHER INFORMATION: includes leader + hfvIIasm + human IgGIFc

US-10-030-203-12_1
SLSLSPGKXXAA1

US-10-030-203-12_2
KLCRDFIMVSQALRILCLLLGLQLCLAAGGVAKASQGGETRDMPWKPGPHRVFVTQEEAHGVLHRRRRANA
FLEELRPGSLERERCKEBCGSFEEAREIFKDAERSYLFWISYSDGDQCASSPCQNGGSCKDGLQSYICFCL
PAFEGRNCETHKDDQLICVNENGGCEQYCSDHTGTKRSCRCHEGYSLLADGVSCTPTVEYPCGKIPILEK
RNASKPQCRIVGGKVCPKGECPWQVLLLVNGAQLCGGTLINTIMVVSAAHCFDKIKNWRNLIAVLGEHDL
SEHDGDEQSRRVAQVIIPSTYVPGTTNHDIALLRLHQPVVLTDHVVPLCLPERTFSERTLAFVRFSLVSG
WGQLLDRGATALELMVLNVPRLMTQDCLCQQSRKYGDSPNITEVMFCAGYSDGSKDSCAGDSGGPHATHYR
GTWYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLQKLMRSEPRPGVLLRAPFPGSAEPRKSCDKTHTCPPC
PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST
YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREXQVYTLPPSRDELTKNQVSLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK

US-10-030-203-12.1
OTHER INFORMATION: hfvIIasm + human IgGIFc

US-10-030-203-12_3
ALQRFHHGLPGPQAPLPSAWASGLPGCRRGRXGLRRRNTGHAVEAGASQSLRNPGGSPRPAPAPARQRV
PGGAAAGLPGEGVQGGAVLLRGGPGDLQGRGEDEAVLDFLQXWGPVCLKSMPEWGLLQGPAPVLILLPP
CLRGPELXDAQXPADLCERERRLXAVLOXPHGHQOALLSVPRGVLSAGRRGVLHTHSXISMWKNTYSRKK
KQOOTPPRNCCGGQVPQRGVSMAGPVVGEWSSVVWGDPDQHHLGGLRGPLFRQNQELEEPDRGRARPQ
RARRGXAPPAGGAGHHPQHVRPGHHQPRIRRAAPPAPARGPHXPCCAPLPARTDVLXEDAGLRALLIGORL
GPAAGPWRHGPAHGAQRAPADDPGLPAAVTEGGRLPKYHGVHVLCRLLGWQOQLLRGGOWRPTCHPLPG
HVVPDGHRQLGPGLRNRGPLWGHVHQGLPVHRVAAKAHALRATPRSPPASPISRIRRAQILXQNSHMPTV
STXTPGGTVSLPLPPKTQQHPHDLPDPXGHMRGGREPRRPXGQVQLVRGRRGAXCQDRAAGGAVQQHV
PCGQRPRPAPGLAEWXQVQVQLOOSPSPHRENHLQSORAAPRTTGVHPAPIPGXADPGEPGGPGPDLPGQ
RLLSQRHRRGVGEWAAGEQLQDHASRAGLRRLLLPLQQAHRGEQVAAGERLLMLRDAXGSAQPLHAEE
ASPCLRVNDKRP1

US-10-030-203-12_4
AAYHLPGDRERLFCVXWLCRASCITEHEKTFPCCHLLLSTVSLLXRKKEPSESSTGGVVLXLFSGCPLL
SHSTAMSLGXKPLTRQVRLTWFLVSSRDGGRVVTVCXSRGCPLALEMVFSMGAGRALLLETLHLYSLPFSQ
SWCRTVRTLTTRVLLYCSSRGPVLAXCTSTPSTYQLNLTSGGSSWLTSTTTHVTSGVRIEMRVSLGFGGK
RXTDGPPRSSGAGHGGHVXVLSQDLGSADPGNGARRRTPGRGSERMSFCSHSMTWNETLVTTPKWPTVAQP
WPQLTMPVRYHVRKWXAVACGPPYLSPAQOESLLPSEXPAQNMYSVIPGESPTFRDCCRQSWVISRGTLSTMS
SRAVAPRSSSWPQPLTNEKRTKASVLSENVRSGRQRGTTWSVRTTGWMCKRRSSAMSWLVVPGTYVLGMWTC
ATRRLCSSPSCLRRSCSFSTAIRFLQFLLISKQWAAEETTQMVLLRVPPHNXAPFTNNRTCHGHSPLGHTL
PTIRPWGLLAFLPSRIGIFPHGYSTVGVQDTPEASRSYPSWHRQERLVPWNSLGYCSGPFPSTTQISWS
SLCVSQFRPSKAGROKQIXDWSWSLQEPPFWHGLEAHWSPSLXEIQNSFVLSASLKISRASSKEHCSSLH
RAWETMMKSLQS1

US-10-030-203-12_5

RPLIIYPETGRGSSACSGCAEPHASRSMRRRSRPAATCSCCPRXACCRGRSRRSRSPAREAWSCSCSPAAHCS
PTPRRCRWDRSLXPGRSGXPGGSWSAHPGMGAGCTPVVLGAALMLWRWFSRWGLGGLCWRPCTCTPCHSAS
PGAGRXGRXPHGTCCCTAPPAALSWXYAPPRRPRTSXTXPQGLRGSSRPPPRMXPQOSSGRSXGCPWVLGGR
GRLTVPPGVQVLGTVGMCEFCHKIWALRIREMGLAGGLLGVALSAXAFAATRCTGRPWCTPQOSGRPLRSP
GPSXRCPSGTTCPGGGWHVGLHCFPPRSPCCHPSSRHRTCTPXYLGSLPPSVTAAGSPSGSSAGARXAPXA
PGPWRHGIPAAGPRSXPMRSARRPASSQRTSVRAGRGAPHGOXGPRAGAGAGAARCRGWWCPGRTCNXXPA
PPAGSAAHPRRARXGRARPAPRSGGSSSSSXFCRNSGPRRPPRWCXSGSPHTTELHSPTTGPAMDTPLWGTPC
PPOFGLGVCWHPFFLEXVFPHMDIQLWVCRTPRLPAESTPRGTDRSAWCPCGHCSTAHSRRSRSHRSAGH
PCASHSSGPPROGSRYRTCAGPCRSPHSGMDLRHTGPHHCKKSRTASSSPRPXRSPGPPRRSTAPPCT
PSPGSSPAJAPPGTRWRRAGAGRAGRRGLPPGLRRLCEAPASTACPVFLLLRPXRPRLQPGSPEAQAEGRGAX
GPGRPXXNLCKA1

US-10-030-203-12_6
GRLSFTRRQGEALLRVVVVQSIMHHGAXEDVPLLPPALVHGELAVEEEGAVGVQHGRRGLVVVLRLPIAL
PLHGDVAGIEAFDQAGQADLVLGQLIPGWEGGVHLXFSGLPFGFGDGFLDGGMBGGPVGDLALVLLAIQPV
LVQDGEDADHTVRAVVLLLPRLCLGXMHLHAVHVPVELDLRVFVAHVHHACDLRGPGDHEGVLGFWGEE
EDXRSFQEFRCWARWACVSFVTRFGLCGGXWGSQOEDSWAWLXAEHELLQPLDVLGDPGVHPKVAHGCAAL
APADDARQVPRAPVVGGMWASTVPRAGVLAAIRVAGTEHVLRDIWGVSHLPXLLQAVLGHQPGHVEHHEL
QGRGATVQQLAPAADOXBAHEGQRPLRERPFGQAEGHHNVSEDHGLVQAEQORDVVVGGARDVRAGDDDLR
HPPALLIPVVLAEVVLAQHRDQVPPVLDFVETVGRGHDHPDGVDQGPPTQLSSIHQQODLPWTLPFGAHLA
PHNSALGFAGISFFXNRYFSTWIFNCGCAGHPVCCQORVPLVAPTGALGARAVVTAVLLTAAVLVHTDQLVI
LVRLTVPALEGREBAEADIGLLBLVLAGAPILAWTXGTLVIITVRNPEOLRPLRVLEDLPGLLBGALLLLAL
PLQGARPQLLQERVGAPAPVQODAVGFLLGYEDSVRPRLPRHVPCFSSXGLSDPACSQAALKPKQKAEBPE
GLGDHDEISAX1

```
O > O ^
O| |O  Intelligenetics
> O <
```

PseqDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-10-617-619-7.res made by jdeleval on Tue 15 Feb 105 11:34:06-PST.

Query sequence being compared:US-10-617-619-7 (1-232)
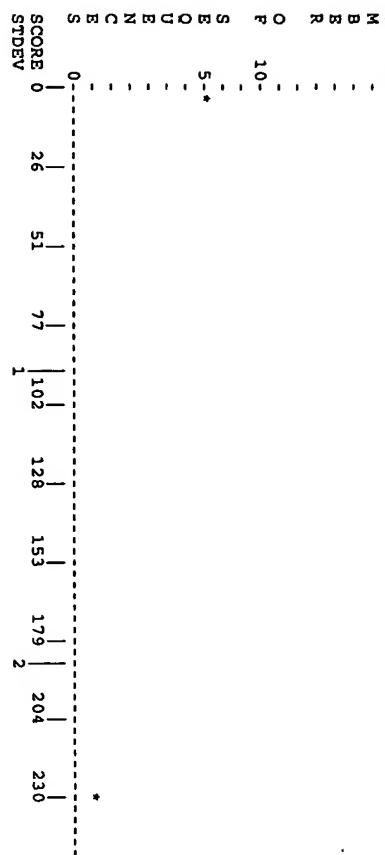Number of sequences being compared: 6
Number of scores above cutoff: 6

Results of the initial comparison of US-10-617-619-7 (1-232) with:
File : trans.pep

```
100-

 N
 U   50-
 M
 B
 E
 R   10-

 O    5-*
 F

 S
 E
 Q    0-
 U
 E    |----|----|----|----|----|----|----|----|----|----|----|----|
 N
 C
 E
 S    *
SCORE  0   26   51   77  102  128  153  179  204  230
STDEV                    1                      2
                                                          *
                                                        230
```

SEARCH STATISTICS

Scores:
	Mean	Median
	43	6

Scores:
	Standard Deviation
	91.61

Times:
	CPU	Total Elapsed
	00:00:00.00	00:00:00.00

PARAMETERS

	Unitary	
Similarity matrix	Unitary	
Mismatch penalty	1	K-tuple	2
Gap penalty	1.00	Joining penalty	20
Gap size penalty	0.05	Window size	32
Cutoff score	0		
Randomization group	0		

Number of residues:
Number of sequences searched: 4270
Number of scores above cutoff: 6   6

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 2 standard deviations above mean ****					
	**** 0 standard deviation from mean ****					
1. US-10-030-203-12	Sequence 12, Application US/10030203	712	230	230	2.04	0
2. US-10-030-203-12		711	7	34	-0.39	0
3. US-10-030-203-12		712	6	32	-0.40	0
4. US-10-030-203-12		711	5	7	-0.41	0
5. US-10-030-203-12		712	5	37	-0.41	0
6. US-10-030-203-12		712	40	5	-0.41	0

1. US-10-617-619-7 (1-232)
   US-10-030-203-12 Sequence 12, Application US/10030203

Sequence 12, Application US/10030203
GENERAL INFORMATION:
APPLICANT: Zhiwei Hu
APPLICANT: Alan Garen
TITLE OF INVENTION: Neovascular-Targeted Immunoconjugates
FILE REFERENCE: OCR-6793.US
CURRENT APPLICATION NUMBER: US/10/030,203
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: PCT/US00/16481
PRIOR FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: MS DOS

SEQ ID NO 12
LENGTH: 2138
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: CDS
OTHER INFORMATION: hFVIIasm immunoconjugate
OTHER INFORMATION: Includes leader + hFVIIasm + human IgG1Fc

Initial Score	=	230	Optimized Score	=	230	Significance	=	2.04
Residue Identity	=	99%	Matches	=	230	Mismatches	=	2
Gaps	=	0	Conservative Substitutions	=	0	Mismatches	=	2

```
            10        20        30        40        50        60        70
KLCRDPIMVSQALRLLCLLLGLQGCLAAGGVAXASGGETRDMPWKPGPHRVPVTQEEAHGVLHRRRRANAFL
            10        20        30        40        50        60        70

            80        90       100       110       120       130       140
EELRPGSLERECKEEQCSFEEAREIFKDAERTKLFWISYSDGDQCASSPCQNGGSCKDQLQSYICFCLPAFE
            80        90       100       110       120       130       140

           150       160       170       180       190       200       210
GRNCETHKDDQLICVNENGGCEQYCSDHTGTKRSCRCHEGYSLLADGVSCTPTVEYPCGKIPILEKRNASKP
           150       160       170       180       190       200       210

           220       230       240       250       260       270       280
QGRIVGGKVCPKGECPWQVLLLVNGAQLCGGTLINTIWVSAAHCFDKIKNWRNLIAVLGEHDLSEHDGDEQ
           220       230       240       250       260       270       280

           290       300       310       320       330       340       350
SRRVAQVIIPSTYVPGTTNHDIALLRLHQPVVLTDHVVPLCLPERTPSERTLAFVRFSLVSGWGQLLDRGAT
           290       300       310       320       330       340       350

           360       370       380       390       400       410       420
ALELMVLNVPRLMTQDCLQQSRKVGDSPNITEYMFCAGYSDGSKDSCAGDSGGPHATHYRGTWYLTGIVSWG
           360       370       380       390       400       410       420

           430       440       450       460       470       480       490
QGCATVGHFGVYTRVSQYIEWLQKLMRSEPRPGVLLRAPFPGSASPKSCDKTHTCPPCPAPELLGGPSVFLF
           430       440       450       460       470       480       490
                                        X         BPKSCDKTHTCPPCPAPELLGGPSVFLF
                                                  ||||||||||||||||||||||||||||

            10        20        30        40        50        60        70        80        90       100
PPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
PPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN
           510       520       530       540       550       560       570

           110       120       130       140       150       160       170
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP
```

```
             580      590      600      610      620      630      640
|||||||||||||||||||||||||||||||||||
GKEYKCKVSNKALPAPIEKTISKAKGQPREXQVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP
|||||||||||||||||||||||||||||||||||
ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
             650      660      670      680      690      700      710
```

2. US-10-617-619-7 (1-232)
   US-10-030-203-12

Initial Score = 7 Optimized Score = 34 Significance = -0.39
Residue Identity = 19% Matches = 46 Mismatches = 140
Gaps = 46 Conservative Substitutions = 0

```
             10       20       30       40       50       60       70
ALQRFHHGLPGPQAPLPSAWASGLPGCRGRGRXGLRRRNTGHAVEAGASQSLRNPGGSPRRPAPAPARQRVPG
             80       90       100      110      120      130      140
GAAAGLPGEGVQGGAVLLRGGPGDLQGRGEDEAVLDFPLQXWGPVCLKSMPEWGLLQGPAPVLYLLLPPCLRG
             150      160      170      180      190      200      210
PELXDAQGXPADLCERERRLXAVLQXPHGHQALLSVPRGVLSAGRRGVLHTHSXISMWKNTYSRKKKCQQTP
             220      230      240      250      260      270      280
RPNCGGQGVPQRGVSMAGPVVGEWSSVVWGDPDQHILGGLRGPLFRQNOELBEPDRGAGRARPQRARRGXAE
             290      300      310      320      330      340      350
PAGGAGHHPQHVRPGHHQPRHRAAPPAPARGPHXPCGAPLPARTDVILXEDAGLRALLIGQRLGPAAGPWRHG
             360      370      380      390      400      410      420      430
PGAHGAQRAPADPQGLPAAVTBGGRLPKYHGVHVLCRLLGWHQQGLLRGGGQWRPTCHPLPGHVVPDGHRQLGP
```

X
E

```
             10       20       30       40       50       60
GLRNRGPLWGVHQGLPVHRVAAKAHALRATPRSPPASPISRIRRAQILXQNSHMPTVPSTXTPGGTVSLPLP
             440      450      460      470      480      490      500
PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC----VVVDVSHEDPEVKFNWYVDGVEV
             10       20       30       40       50       60
PKTQGHPH--DLPDPXGHMRGG--GRRPRRPKGQVQLVRGRRGGAXCQDKAAGGAVQQHVP--------CGQRP
             510      520      530      540      550      560
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA-------LPAPIEKTISKAKGQPREPQVY
             70       80       90       100      110      120      130
HRPAPGLAEWQ-----GVQV-QGLQQQSPPSPHRENHLQSGQRAAPRTTGVHPAPIPGXADQEPGGQPDLPGQR
             570      580      590      600      610      620      630
TL-------PESRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL-DSDGSFFLYSKL
             140      150      160      170      180      190
LLSQRHRRGVGEQWAAGEQLQDHASRAGLRRLLLPLQQA---HRGQBQVAAGERLLMLRDAXGS---AQPL
             640      650      660      670      680      690
```

3. US-10-617-619-7 (1-232)
   US-10-203-12

```
             200      210      220      230
             X
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
HABRPLPVSGXMISG
             700
```

Initial Score = 6 Optimized Score = 32 Significance = -0.40

```
             200      220      230
             X
```

Residue Identity = 19% Matches = 45 Mismatches = 143
Gaps = 45 Conservative Substitutions = 0

```
             10       20       30       40       50       60       70
SFAEISSWSRPSGSSAPCLGFRAAWLQAGSLRPQEEKHGTCRGSRGLTESSXPRRKPTASCTGAGAPTRSW
             80       90       100      110      120      130      140
RSCGRAPWRGSARRSAPSRRPGRSSRTRRGRSCSGFLTVWGTSVPQVHARMGAPARTSSSPISASASLPSR
             150      160      170      180      190      200      210
AGTVRRTRMTSXSVXRTAAVSSTAVTTRRAPSAPVGATRGTLCWQYGCPAHPQLNIHVEKYLFXXCQMPANP
             220      230      240      250      260      270      280
KAELWGARCAPKGSVHGRSCCWXMELSCVGGPXSTPSGWSPRPTVSTKSRTGGGTXSRCWASTTSASTTGMSR
             290      300      310      320      330      340      350      360
RAAQPWATLGCTPGSPSTSSGCCKSSCSCAQSHAQEBSSCEPHFPDPQSPNLVTKLTHAHRAQHLNSWGDIQQSSSS
             440      450      460      470      480      490      500
PWSSWCSTCPGXXPRTACSSHGRWETPQISRSTCSVPATRMAARTPARGTVBAHMPPTTGARGTXRLSSAGA
             370      380      390      400      410      420      430
             X       10
             EPKSCDKTHTC
             10       20       30       40       50       60       70
PPCP-APELLGGP--SVFLFPPKPKDTLMISRTPEVT---CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
             510      520      530      540      550      560
PQNPRTPSXSPGFLRSHAWWMTXATKTLRSSSTGTWTAWRCIXPRQS------RGRSSTTARTVWSA--SSPS
             80       90       100      110      120
BEQYNSTYRVVS--VLTVLHQDWLNGKEYKCKVS------------NKALPAPIEKTISKAKGQP
             570      580      590      600      610      620      630
CTRTGXMARGTSARSPTKPSQPPPSRKPSPKGSPENXRCTPCPHPGMSXPRTRSAXPA------WSCASIPA
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
             200      210      220      230
VNDKRP
             710      X
```

4. US-10-617-619-7 (1-232)
   US-10-030-203-12

Initial Score = 5 Optimized Score = 7 Significance = -0.41
Residue Identity = 16% Matches = 7 Mismatches = 35.
Gaps = 0 Conservative Substitutions = 0

```
             10       20       30       40       50       60       70
EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGYEVHNA
             80       90       100      110      120      130      140
KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT
             150      160      170      180      190      200      210
KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
             X
GRLSFTRRQGEALLRVVVVQSLMHHG
             10       20
             220      230      X
```

```
LHNHYTQKSLSLSPGK
AXEDVPLLPPALVHGELAVEEEGAVGVGVQOHGRGRGLIVVLRLPIALPLHGDVAGIEAFPDQAGQADILVLGQLIPG
  30        40 X        50        60        70        80        90
WGGGVHLXPSGLPFGRGDGFLDGGWEGFVGDLALVLLAIQPVLJVQDGEDADHTVRAVLLLPRLCLGXMHLH
100       110       120       130       140       150       160       170
AVHVPVELDLRVFVAHVHHHACDLRGPGDHEGVLGFWGBEEDXRSPQEFRCWARWACVSFVTRFGLCGSGKW
180       190       200       210       220       230       240
GSQEDSWAWLXAHELLQPLDVLGDPGVHPKVAHGCAALLAPADDARQVPRAPVVGGMWASTVPRAGVLAAIRV
250       260       270       280       290       300       310
AGTEHVLRDIWGVSHLPXLLQAVLGHQPGHVBHHELQCRGATVQQLAPAADQXEAHEGQRPLRERPFGQOABG
320       330       340       350       360       370       380
HHMVSEDHGLIVQAAEQRDVVVGGARDVRAGDDDLRHPPALLIPVVLAEVVLAQHRDQVPPVLDFVETVGRGDH
390       400       410       420       430       440       450
FSSXGLLSDPACSQAALKPKQKAAEPEGLGDHDEISAK
680       690       700       710
```

```
RPLIIYPETGRGSSACSGCABPHASRSMRRRSPAATCSCPRXACCRGRRSRRSPAREAWSCSCCSPAAHCSPT
       10        20        30        40        50        60        70
PRRCRWDRSLXPdRsGXPGSWSAAHPGMGAGCTPVVLGAALWLWRWPSRWGLGGSLCWRPCTCTPCHSASPGAG
        80        90       100       110       120       130       140
RXGRXPEHGTCCCTAPPAALSWXYAPPRRRPRTSXTXPQGLRGSRPPPRMXPQGSGRSXGGCPWVLGGRGRLTVP
        150       160       170       180       190       200       210
PGVQVLGTVGMCEFCHKIWALRIREMGLAGGLLGVALLSAXAFAAATRCTGRPWCTPQSGPRLRSPGSXRCPS
220       230       240       250       260       270       280
GTTCPGSGGWHVGLHCPPRSPCCHPSSRHRTCTPXYLGSLPPSVTAAGSPGSSAGARXAPXAPGPWRHGPAA
290       300       310       320       330       340       350       360
GPSRXPMRSARRPASSQOFTSVRAGRGAPHGQXGPRAGGAAARCRGWNCPGRTCWGXXPAPPAGSAHPRRAR
370       380       390       400       410       420       430
```

```
LRXVFFRMDIQLMVCRTFPRLPAESTPRGTDRSAWCP            CGHCSTAHSR            RSRSHRS
510       520       530       540            550
VLH--QDWLNGKEYKCKVS---NKALP--AP----                 IEKTISKAKGQPREPQVYTLPPSR---DE
100       110       120       130       140
```
```
    30        40        50        60        70        80        90
----PPKPKDTLMISRTP----EVTLCVVDVSHEDPEVKRFNWYVVDGVEVHNAKTPREEQYNSTYRVVSVLT
XGRARPAPRSGGSSSSSXFCRNSGPRRPPRWCXSGGSPHTTELHSPTTGPAMDTPLLWGTPCPPQFGLGVCMHFFF
440       450       460       470       480       490       500
```

```
AGHPCCASHSSGGPRRQGGRRSRYRTCGAGPGCRSPHSGGMDLRHTGPHHCCKKSRTASSSPR-PXRSPGGPPRRSTAPP
560       570       580       590       600       610       620
LTKNQVSLTCLVXGPYPSDIAVEWESNGQP-----ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF
150       160       170       180       190       200
CTPSGPSPAAAPGGTRWRAGAGACRRGLPPGLRRLCBAPASTACPV------FL--LLRPXRPRLQOPGSPB
630       640       650       660       670       680       690
SCSVWHEALLHNHYTQKSLSLSPGK
210       220       230
AQABGRGAXGPGRRXXNLCKA
700       710 X
```

```
AAAYHLPGDRERLFCVXXMLCRASCITTEHRKTFPCCHLLLSTVSLLXRKKSKPSESSTGGVVLXLFSGCPLLSH
       10        20        30        40        50        60        70
STAMSLGXXPLTRQVRLTMWFLVSSSRDGGRVYTCXSRGCPLALEMVFSMGAGRALLETLHLYSLLPPSQSWCR
        80        90       100       110       120       130       140
TVRTLTTRVVLLYCSSRGFVLAXCTSTPSTYQLNLTSGSSWLTSTTTHVTSGVRBIMRVSLGFGGKRKTDGP
150       160       170       180       190       200       210
PRSSGAGHGGHVAXVLSQDLGSADPGNGARRRTPGRGSERMSFCSHSMYWETLLVYTPKWPFVAQPWPQLTMPV
220       230       240       250       260       270       280
RYHVPRXWVACGPPLSPAQESLLPSEXPAQNMYSVIFGBSSPFTRDCCRQSWVISRGTLSTMSSSRAVAPRSSS
290       300       310       320       330       340       350       360
```

```
    10        20
X
EPKSCDKTHTCP-------PCPAPELLGGPSVF
WPQPLTNBKRTKASVLSENVRSGRQRGTTWSVRTTGWCRRSSAMSWLVVPGTYVILGMYCATRRLCSSPSCS
370       380       390       400       410       420       430
LFPPKP------KDTLMIS--RTPEVTCVVVDVSHEDPEVKRFNWYVVDGVEVHN--AKTKPREEQYNS----
30        40        50        60        70        80
LRSCSPSTAIRFLQFLILSKQWRAABTTQMV------LIRVPPHNXAPFTNNRTCHGHSPLGHT
440       450       460       470       480
```

```
    90        100       110       120       130       140       150
---TYRVVSVLTVLHQDWLNGKEYKCKVYSNKALPAPIEKTISRAKGQPREPQVYTL-PPSRDELTKNQVSLT
SLCVSQOFPRSKAGRQKQIXDWSWSLQEPPFWHGLEAHWSPSLAXEIQNSFVLSASL--KISR--ASSKEHCSS
570       580       590       600       610       620
LPPIIRPWGLLAFLFSRIGIFPHGYSTVGVQDTPSASRBYPS--WHRQERLVPWSLQYCSQPPFSFTQ1SWS
490       500       510       520       530       540       550       560
```

```
    160       170       180       190       200       210
CL--VXGFYPS-----DIAVEWESNGQP---ENNYKTTPPVL-DSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK
220       230 X
LH------SLSREPGRSSSRNALARRRCRTPWASSWTVKTLXGPGFHGMSRVSPPEALLATFPAARQP
630       640       650       660       670       680       690
XSPSRRQRSLRAWBTMMKSLQS
700       710
```

```
> O <
O | O   IntelliGenetics
> O <
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-10-617-619-8.res made by jdelaval on Tue 15 Feb 105 11:34:34-PST.

Query sequence being compared:US-10-617-619-8 (1-641)
Number of sequences searched: 6
Number of scores above cutoff: 6

Results of the initial comparison of US-10-617-619-8 (1-641) with:
File : trans.pep

```
 N  100-
 U
 M   50-
 B
 E
 R
 O   10-
 F
 S    5*
 E
 Q
 U
 E
 N
 C
 E
 S    0-   *                                                   *

SCORE 0   71   142   213  |284   354   425   496| 567   638
STDEV                     | 1                 2 |
```

PARAMETERS

	Unitary	
Similarity matrix	Unitary	
Mismatch penalty	1	K-tuple
Gap penalty	1.00	Joining penalty
Gap size penalty	0.05	Window size
Cutoff score	0	
Randomization group	0	

K-tuple		2
Joining penalty		20
Window size		32

SEARCH STATISTICS

	Mean	Median	Standard Deviation
Scores:	113	9	257.12

Times:

	CPU	Total Elapsed
	00:00:00.00	00:00:00.00

Number of residues:		4270
Number of sequences searched:		6
Number of scores above cutoff:		6

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 2 standard deviations above mean ****					
	**** 0 standard deviation from mean ****					
1. US-10-030-203-12	Sequence 12, Application US/10030203	712	638	638	2.04	0
2. US-10-030-203-12		712	11	60	-0.40	0
3. US-10-030-203-12		711	8	39	-0.41	0
4. US-10-030-203-12		712	8	57	-0.41	0
5. US-10-030-203-12		711	7	98	-0.41	0
6. US-10-030-203-12		712	7	42	-0.41	0

---

1. US-10-617-619-8 (1-641)
   US-10-030-203-12 Sequence 12, Application US/10030203

Sequence 12, Application US/10030203
GENERAL INFORMATION:
APPLICANT: Alan Garen
APPLICANT: Zhiwei Hu
TITLE OF INVENTION: Neovascular-Targeted Immunoconjugates
FILE REFERENCE: OCR-6799B.US
CURRENT APPLICATION NUMBER: US/10/030,203
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: PCT/US00/16481
PRIOR FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: MS DOS
OTHER INFORMATION: Includes leader + hfVIIasm + human IgGIFc
SEQ ID NO 12
  LENGTH: 2138
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  NAME/KEY: CDS
  OTHER INFORMATION: hfVIIasm immunoconjugate
  OTHER INFORMATION: Includes leader + hfVIIasm + human IgGIFc

Initial Score	=	638	Optimized Score = 638 Significance = 2.04
Residue Identity	=	97%	Matches = 628 Mismatches = 13
Gaps	=	0	Conservative Substitutions = 0 STDEV = 0

```
                                                                    X
                                                                 ANAFL
                                                                 |||||
      KLCRDFIMVSQALRLLCLLLGLQGCLAAGGVAKASGGETRDMPWKPGPHRVFVTQEEAHGVLHRRRANAFL
            10        20        30        40        50        60        70

       10        20        30        40        50        60        70
      XXLRPGSLXRXCKXXQGSFXXARXIIFXDAXRTKLFWISYSDGDQCASSPCQNGGSCKDQLQSYICFLPAFE
      ||||||    |||     |  |  ||||||  |||||||||||||||||||||||||||||||||||||||
      EELRPGSLERECKEEQCGFPEEARSIFKDAERTKLFWISYSDGDQCASSPCQNGGSCKDDLQSYICFLPAFE
            80        90        100       110       120       130       140

       80        90        100       110       120       130
      GRNCETHKDDQLICVNENGGCEQYCSDHTGTKRSCRCHEGYSLLADGVSCTPTVEYPCGKIPILEKRNASKP
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      GRNCETHKDDQLICVNENGGCEQYCSDHTGTKRSCRCHEGYSLLADGVSCTPTVEYPCGKIPILEKRNASKP
            150       160       170       180       190       200       210

       150       160       170       180       190       200
      QGRIVGGKVCPKGECPWQVLLLVNGAQLCGGTLINTIWVVSAAHCFDKIKNWRNLIAVLGEHDLSEHDGDEQ
      |||||   |||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      QGRIVGGKVCPKGECPWQVLLLVNGAQLCGGTLINTIWVVSAAHCFDKIKNWRNLIAVLGEHDLSEHDGDEQ
            220       230       240       250       260       270       280

       230       240       250       260       270       280
      SRRVAQVIIPSTYVPGTTNHDIALLRLHQPVVLTDHVVPLCLPERTFSERTLAFVRFSLVSGWGQLLDRGAT
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      SRRVAQVIIPSTVPGTTNHDIALLRLHQPVVLTDHVVPLCLPERTFSERTLAFVRFSLVSGWGQLLDRGAT
            290       300       310       320       330       340       350

       290       300       310       320       330       340       350       360
      ALELMVLNVPRLMTQDCLQQSRKVGDSPNITEYMFCAGYSDGSKDSCKGDSGGPHATHYRGTWYLTGIVSWG
            360
```

```
                          370             380             390             400             410             420             430
ALELMVLANVPRLMTQDCLQQSRKVGDSPNITBYMFCAGYSDGSKDSCAGDSGGGPHATHYRGTWTLTGIVSWG
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QGCATVGHFGVYITRVSQYIEWLQKLMRSEBPRPGVLLRAPPFGSAEPKSCDKTHTCPPCPAPELLGGPSVFLF
                          370             380             390             400             410             420             430

                          440             450             460             470             480             490             500
QGCATVGHFGVYITRVSQYIEWLQKLMRSEBPRPGVLLRAPPFGSAEPKSCDKTHTCPPCPAPELLGGPSVFLF
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN
                          440             450             460             470             480             490             500

                          510             520             530             540             550             560             570
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GKEYKCKVSNKALPAPIEKTISKAKGQPREXQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP
                          510             520             530             540             550             560             570

                          580             590             600             610             620             630             640
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                          580             590             600             610             620             630             640

                          650             660             670             680             690             700             710
ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKXXXAA
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                          X
```

2. US-10-617-619-8 (1-641)
   US-10-030-203-12

Initial Score =	11	Optimized Score =	60	Significance =	-0.40
Residue Identity =	17%	Matches =	77	Mismatches =	299
Gaps =	72	Conservative Substitutions =	0		

```
                10             20             30             40             50             60             70
ANAFLXXLRPGSLXRXCKXXQCSFXXARXIFKDAXRTKLFWISYSDGDQCASSPCONGGSCKDQLQSYICFC
|              |    |      ||    |  |    |        ||      |  |    |
LPAFEGRNCETHKDDQLICVNENGCGCEQYCSDHTGTKRSCRCHEGYSLLADGVSCTPTVEYPCGKIPILEKR
                80             90             100            110            120            130            140

                150            160            170            180            190            200            210
NASKPQGRIVGGKVCPKGECPWQVLLLVNGAQLCGGTLINTIWVVSAAHCFDKIKNWRNLIAVLGEHDLSEH
        |       |            |         |  |   |       |  |
DGDEQSRRVAQVIIPSTYVPGTTNHDIALLRLHQPVVLTDHVVPLCLPERTFSERTLA--FVRFSLVSGWGQ
                220            230            240            250            260            270            280

                290            300            310            320            330            340            350
RPLIIYPETGRGSSACSGCAEP--HASRSMRRRSPAATCSCPRXACCRGRRSRRS----
        X       10             20             30             40             50
-PAREAWSCSCSPAAHCSPTPRRCRWD---RSLXPGRSGXPGSWSAAHPGMGAGCTPVVLGAAALLMRWFSR-
LLDRGA-----TALELMVLANVPRLMTQDCLQQSRKVGDSPNITBYMFCAGYSDGSKDSCSCKGDSGGGPHATHYRG
                60             70             80             90             100            110            120

                360            370            380            390            400            410
TWYLTG--------IVSWGQGCATVGHFG--VYTRVSQYIEWLQKLMRSEBPRPGVLLRAPPFGSAEPK
|                |                  |
-WGLGGLCWRPCTCTPCHSASPGAGRXGRXPKPHGTCCCTAPPAALSWXXYAPPR-RPRTSXTXPQGIRGSRPPP
                130            140            150            160            170            180            190

                420            430            440            450            460            470            480
SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT-
RMXPQGSGRSGXGCPWVLGGRGRLTVPPGVQVLGTVGMCEFCHKIWALRIREMGLAGGLLGVALSAXAFAATR
                200            210            220            230            240            250            260

                490            500            510            520            530            540
-KPRREEQYNSTYRVVSVLTYLHQDWLNGKBYXCKCVSNKALPAPIEKTISKAKGQPREPQVYT
--------KPRREEQYNSTYRVVSVLTYLHQDWLNGKBYXCKCVSNKALPAPIEKTISKAKGQPREPQVYT
                490            500            510            520            530            540
```

```
                270            280            290            300            310            320
CTGRPWCTPQSGPRLRSPGPSXRCPSGTTCPGSGWHVGLHCPPRRSPCCHP-------SSRHRTCTPXYLGS
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QGNVFSCSVMHBALHNHYTQKSLSLSPGK
XG-------PRAGAGAAARCRGWWCPGPGRTCWGXXPAPPAGSAHPRRARXGRARFAPRSGSSSSXFGRNSGP
                                                    X
                400            410 X          420            430            440            450

                460            470            480            490            500            510            520
RRPPPRWCXXSGSSPHTTELHSPTTGPAMDTPLWGTPCPPQFGLGVCWHFFFLLEXVFFHMDIQLWVCRTPRLPAB
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR----WQ
                550            560            570            580            590            600            610

                530            540            550            560            570            580            590
STPGTDRSAWCPCGHCSTAHSRSRSHRSAGHPCASHSSGPRROQGRSRYRTGAGPCRSPHSGMDLRHTGP
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
LPPSVTPAAGSPGSS-----AGARAPXPAPGPWRHG-PAAGPSRXF--MRSARRPASSQRTSVRAGRGAPHGQ
                330            340            350            360            370            380            390

                600            610            620            630            640            650            660
HHICKSRTASSSPPRPXRSPGPPRRSTAPPCTPSPGSSPAAAPPGTRWRAGAGAGRGLPPGLRRLCEAPASTA
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CPVFLLLRPXRPRLQPGPGSPERAQAEGRGAXGPGRPXXNICKA
                680            690            700            710
```

3. US-10-617-619-8 (1-641)
   US-10-030-203-12

Initial Score =	8	Optimized Score =	39	Significance =	-0.41
Residue Identity =	21%	Matches =	53	Mismatches =	149
Gaps =	50	Conservative Substitutions =	0		

```
                10             20             30             40             50             60             70
GRLSPTRRQGEALLRVVVVQSLMHIGAXEDVFLLPPALVAIGELAYBEEGAVGVQHORRGLVVVLRLPIALPL
|       |           |      ||    |    |     |    ||       |    |      |
HGDVAGIEAFDQAGQOADLVLGOLIPGWGQGVHLLXFSGLPGFGPDGFLDGGWEGFVGDLALVLLAIQPVLVQD
                80             90             100            110            120            130            140

                150            160            170            180            190            200            210
GEDADHTVRAVVLLLPRICLGXMHLHAVHYPVELDLRVFVAHVHHHACDLRGPGHGDHEGVLGPWGEEBDXRSP
|                  |                    |
QBFRCWARWACVSFVTRFGLCGGSGKWGSQEDSWAWLXAHELLQPLDVIGDPGVHPRKVAHGCAAALAPADDARQ
                220            230            240            250            260            270            280

                290            300            310            320            330            340            350
VPRAPVVGGWWASTVPRAGYVLAAIRVAGTHVLRIDTWGVSHLPXLLQAVLCHQPGHVEHHELQGRGATVQQL
|       |                |
APAADCXEAHEGQRPLRERPFGQAEGHHMVSBDHGLVQAFORDVAVVGGARDVRAGDDDLRHPPALLIPVVLA
                370            380            390            400            410            420            430

                440            450            460            470            480 X          490            500
EVVLAQHRDQVPPVLDFVETVGRGDHPDGVDQGPPTQLSSIHQQODLPWTLPFGAHLAP--HNSALCGFAGIS
|                      |                           X
FXXXAR-----XIF------KDAXRTKLFWISYSDG--DQCASSPCONGGSCKDQLQSYICFCLPAFEGRNC
                30             40             50             60             70             80

                510            520            530            540            550            560            570
FPXNRYFPSTWIFNCCGAGHPVCQQRVPLVAPTGALGARVTAVLLTAAVLVHTDQLVILVRLTVPALEGREA
|                    |                    |  |
ETHKDDQL-----ICVNENGGCEQYCSDHTGTKRSCRCHEGYSLLADGVSCTPTVEYPCGKIPIL--EKRN
                90             100            110            120            130            140

                580            590            600            610            620            630            640
BADIGLELVLAGAPILAWTXGTLVIPITVRNPEQLRPLRVLEDLPGLLEG-ALLLLALPLQGARPQLLQBRVG
|                                                |
                150            160            170            180            190            200            210
```

4. US-10-617-619-8 (1-641)
   US-10-030-203-12

Initial Score	=	8
Residue Identity	=	21%
Gaps	=	67

Optimized Score	=	8
Matches	=	81
Conservative Substitutions	=	57

Significance	=	-0.41
Mismatches	=	222
	=	0

```
AAAYHLPGDRERLFCVXWLCRASCITEHEKTPPCCHLLLSTVSLLXRKEEPSESSTGGVVLLXLFSGCPLLSH
         10        20        30        40        50        60        70

STAMSLGXKPLTRQVRLTWFLVSSSRDGGRRVYTCXSRGCPLLALEMVFSMGAGRALLETLHIYSLPFSQSWCR
         80        90       100       110       120       130       140

TVRTLTTRYVLLYCSSRGFVLAXCTSTPSTYQLNLTSGSSWLTSTTTHVTISGVREIMRVSLGFGGRKRTDGP
        150       160       170       180       190       200       210

PRSSGAGHGGHVXVLSQDLGSADPGNGARRRTPGRGSERMSFCSHSMYWETLVYTPKWPTVAQPWPQLTMPV
        220       230       240       250       260       270       280

RYHVPRXWVACGPPLSPAQESLLPSEXPAQNMYSVIPGESSPTFRDCCRQSWVISRGTRLSTMSSRAVAPRSSS
        290       300       310       320       330       340       350

WPQPLTNBKRTKASVLSENVRSG-RQRGTTWSVRTTGWCR--RSSAMSWLVVPGTYVLGNWMTCATRRLCSSP
        360       370       380       390       400       410       420

CQNGGSC--;--KDQLQSYICFCLPAFBGRNCETHKDDQLICVNENGGCEQYCSDHTGTKRSCRCHBGYSLL
         430       440       450       460       470       480

ADGVSCTPTVEYPCGKIPILBKRNASKPQG-RIVGGKVC---KGGCP--WQVLL-LVNGAQLC----GGT
         490       500       510       520       530       540

QI--SWSSLCVSQFRPSKAGRQKOIXDWSWSLQEPPFWHGLE----AHWSPSLXBIONSPVLSASLKISR
         550       560       570       580       590       600       610
```

5. US-10-617-619-8 (1-641)
   US-10-030-203-12

Initial Score	=	7
Residue Identity	=	19%
Gaps	=	143

Optimized Score	=	98
Matches	=	139
Conservative Substitutions	=	143

Significance	=	-0.41
Mismatches	=	418
	=	0

```
ALQRFHHGLPGGPQAPLPSAWASGLPGCRRGRXGLRRRNTGHAVEAGASQSLRNPGGGSPRRPAPAPAQRVPG
         10        20        30        40        50        60        70

GAAAGLPGEGVQGGAVLLRGGPGDLQGRGEBDEAVLDFLQXWGPVCLKSMPEWGL-LQGGPAPVLYLLI-PPCLR
         80        90       100       110       120       130       140

GGSCKDQLQSYICFCLPAFEGRNCETHKDDQLICV-NENGGCEQYCSDHTGTKRSCR---CHEGYSLLAD
         60        70        80        90       100       110       120

GPELXD-----AQGKPA---DLCE--RERRLXAVLQXPHGHQALLSVPRGVLSAGRRGVLHTHSX SMWKN
        130                          140       150       160       170       180

TYSRKCKKCCQQTPRPNCG-GQGVPQRGVS-MAGPVVGEWSSVVWGDPDQHHLGGLRGPLFRQNQELERPDRGA
        210       220       230       240       250       260       270

GRARPQRAARGXAEPAGGAGHHPQHVRPGHHQPRHRAAPPAPARGPHXPCCGAPLRARTDVLXEDAGURALLI
        280       290       300       310       320       330       340

--RLHQPVVLTDHVVPLCLPBRTFSBRTLAFVRFSLVSGWGQLLDRGATALLELMVL-----NVPRLMTQDCLQ
        250       260       270       280       290       300       310

GORL-----GPAAGPWRHGPGAHGAQRAPADDPG----LPAAVT--EGGRLPKYHGVHVLCLLGWQ
        350       360       370       380       390       400

QI-LLRCGQWRPT----CHPLPGHVVPDGHRQLGP-GLRNRG--PLWG-VHQGLPVHRVAAKAHALRATPRS
        410       420       430       440       450       460
```

```
6. US-10-617-619-8 (1-641)
   US-10-030-203-12

   Initial Score  =   7     Optimized Score  =   42    Significance  =  -0.41
   Residue Identity =  19%   Matches          =   62    Mismatches    =   187
   Gaps            =  70     Conservative Substitutions =  0

                10        20        30        40        50        60        70
   SFAEISWSWSPRSGSSAFCLGFRAAWLQAGSLRPQEEKHGTCRGSRGLTESSXPRRKPTASCTGAGAPTRSW
            10        20        30        40        50        60        70

   RSCGRAPWRGSARRSSAPSRRPGRSSSRTRRGRRGRCSGFLTVMGTSVPQVHARMGAPARTSSSPISASALPSR
            80        90        100       110       120       130       140

   AGTVRTRMTSXSVXTRRAAVSSTAVTTRAPSAPVGATRGTLCWQTGCPAHPQLNIHVEKYLPXKXKEMPANP
            150       160       170       180       190       200       210

   KAELWGARCAPKGSVHGRSCCWXMELSCVGGGYXSTPSGWSPRPTVSTTKSRTGGTVXSRCWASTTSASTTGMSR
            220       230       240       250       260       270       280

   AGGWRRSSSPARTSRAPPTTTSRCSACTSPWSSLTMWCPSACPNGRSLRGRWPSCASHWSAAGASCWTVAPR
            290       300       310       320       330       340       350

   PWSWSCSTCPGXXPRTACSSHGRWETPOISRSTCSVPATRMAARTPARGTVEAHMPPTTGARGTXRASSAGA
            370       380       390       400       410       420       430

   RAAQPWATL-GCTPGSPSTSSGCK-SSCAQSHAQBSSCBPHFPDPQSNLVTKL---THAHRAQHLNSWGDR
            440       450       460       470       480       490

   GGSCKDQ-LQSYICFCLPAFBGRNCETHKDDQLICVNENGGCEQYCSDHTGTKRSCRC-----HEGYS-LLA
            60        70        80        90        100       110       120

   QSSSSPQNPRTPSXSPGPLRSHAWWTXATKTL-----RSSSTGTWTAWRCIXPRQSRGRSSTTA
            500       510       520       530       540       550

   DGV------SCTPTVEYPCGKIPILEKRNASKPQGRIVGGKVCPKGBCPWQVLLVNGAQLCGGTLINTIWV
            130       140       150       160       170       180

   RTVWSASSPSCTRT-GXMARSTSARSPTKPSQPPSRKPSPK--PKG---SPENXRCTCPHPGMSXPRT---
            560       570       580       590       600       610       620

                190       200       210       220       230       240       250
```

Right column:

```
   VSAAHCFDKIKNWRNLIAVLGEHDLSEHDG-DEQSRRVAQVIIPSTYVPGTTNHDIA--LLRLHQPVVLTDH
   RSAXPAWSK----------------ASIPATSPWSGRAWGSRRTTRPRLPCWTPTAPSSSTASSPWTRAGGSRGTSS
            630       640       650       660       670       680

   VVPLCLPERTFSERTLAFVRFSLVSGWGQLLDRGATALELMVLANVPRLMTQDCLQQSRKVGDSPNITEYMPC
            270       280       290 X     300       310       320

   HAPXCMRLCTTTTRRA-------SPCLRVNDKRP
   690               700       710 X

   DGVEVHNAKTKPREEQYNSTYRVSVLITVLHQDMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVTL
   330       340       350       360       370       380       390       400

   AGYSDGSKDSCKGDSGSGGPHATHYRGTWYLTGIVSWGQGCATVGHPGVYTRVSQYIEWLQKLMRSBPRPGVLL
            410       420       430       440       450       460       470

   RAPPPGSAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKPNWYV
            480       490       500       510       520       530       540

   PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF
   550       560       570       580       590       600       610

   SCSVMHEALHNHYTQKSLSLSPGK
   620               630       640
```

Lower-left block:

```
                390       400       410       420       430       440
   ------QYIEWLQKLMRSBPRPGVLLRAPPPGSAEPKSCDKTHTCP----PCPAPELLGGPSVFLFPPKPKDT
   PPASPISRIRRAQILXQNSHMPTVPSTXTPGGTVSLPLPPKTQSHPHDLPDPGHMRGG-GRRPRPRPXGQVQ
   470       480       490       500       510       520       530

                450       460       470       480       490       500       510
   LMISRTPEVTC---VVVDVSHEDPEVKPNWYVDVGVEVHNAKIKPREEQYNSTYRVSVLITVLHQDMLNGKE
   LVRGRRGGAXCQDKAAGGAVQQHVP------CGQRPHRPAPGLAEWQ------GVQV-QGLQQSPPSPHR
   540       550       560       570       580       590

                520       530       540       550       560
   YXCKVSNKA-------LPAPIEKTISKAKGQPREPQVTL---------PPSRDELTKNQVSLTCLVKGFY
   ENHLQSQRAAPRTTGVHRPAPIGXAQQBPGQPDLPGQRLLSQRHRRGVGEQWAAGEQLQDHASRAGLRRLIL
   600       610       620       630       640       650       660

                570       580       590       600       610       620       630
   PSDIAVEWESNGQPENNYKTTPPVL-DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
   PLQQA---HRGQEVAAGBRLLMLRDAXGS---AQPLHAEEPLPVSGXMISG
   670       680       690       700       710

                640
   PGK
```